

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 9, 2002, 17:56:19 ; Search time 2638 Seconds  
(without alignments)  
6385.846 Million cell updates/sec

Title: US-09-635-501-2  
Perfect score: 4291  
Sequence: 1 MSSSSWLLLSLVAVTAAQT.....ISKGNNPGFQNTDDVQTSF 805

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0  
  
Searched: 1797656 seqs, 10463268293 residues  
  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USFPO\_spool/US09635501/runat\_09102002\_094529\_18524/app\_query.fasta\_1.967  
-DB=GenEmbl -OPMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09635501 -ACGN\_1\_1\_1714 -runat\_09102002\_094529\_18524 -NCPU=6 -ICPU=3  
-NO\_XLPAY -NO\_MMAP -LARGOQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THRAIDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4291	100.0	2415	6	ARL35178 Sequence
2	4291	100.0	2415	6	E43987 ACE-analog
3	4291	100.0	2418	6	E39033 MPROT15 pol
4	4291	100.0	2599	6	E43988 ACE-analog
5	4291	100.0	3325	9	AF291820 Homo sapi
6	4291	100.0	3334	6	AX047758 Sequence
7	4291	100.0	3396	6	ARL35177 Sequence
8	4291	100.0	3405	9	AF241234 Homo sapi
9	4288	99.9	2599	9	AB046569 Homo sapi
10	4281	99.8	3341	9	AL10224 Homo sapi
11	3740.5	87.2	2262	6	E39034 MPROT15 pol
12	3579	83.4	2638	6	AX047762 Sequence
13	3562	83.0	2760	10	AB053181 Mus muscu
14	3561	83.0	2638	6	AX047765 Sequence
15	3509	81.8	2415	6	AX047760 Sequence
16	2904	67.7	2415	6	AX047764 Sequence
17	2167	50.5	1993	10	AB053182 Mus muscu
18	1344	31.3	2473	9	HUMTACEA
19	1344	31.3	2477	9	HSACE
20	1344	31.3	2478	6	A31567 H.sapiens t
21	1344	31.3	2478	6	AR037213 Sequence
22	1337	31.2	4020	6	ARL37383 Sequence
23	1337	31.2	4020	9	HUNTAICEB
24	1337	31.2	4024	6	A00914 H.sapiens g
25	1334	31.1	2418	10	MUSACEC
26	1334	31.1	3813	10	MUSACEA
27	1334	31.1	3939	6	AX147531 Sequence
28	1334	31.1	4563	6	AX147503 Sequence
29	1334	31.1	4694	10	MUSACEB
30	1322	30.8	2551	9	HUMTACEC
31	1312	30.6	4050	5	CHKACEI
32	1310	30.5	4014	10	AF201331 Rattus no
33	1310	30.5	4014	10	AF201332 Rattus no
34	1310	30.5	4014	10	U03708 Rattus norv
35	1310	30.5	4142	10	RND03734 Rattus norv
36	1303	30.4	2490	9	HUMTACEB
37	1283.5	29.9	4803	4	OCANCOE
38	1283	29.9	2409	4	RABACEA
39	1099.5	25.6	2211	3	AB026110 Bombyx mo
40	1090	25.4	2001	3	DM025344 Drosophila
41	1086	25.3	2002	3	AY061129 Drosophila
42	1061	24.7	1998	3	DM034599 Drosophila
43	1058	24.7	2664	3	HMBH1PR Haematobia
44	1057	24.6	4387	3	BMU62809 Boophilus m
45	1030	24.0	2452	3	DMACERNET D.melanogas

ALIGNMENTS

RESULT 1  
ARL35178 LOCUS ARL35178 2415 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 3 from patent US 6194556.  
ACCESSION ARL35178  
VERSION ARL35178.1 GI:14124083  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.	
REFERENCE 1 (bases 1 to 2415)	
AUTHORS Acton, S. Laurene and Robison, K. Earl.	
TITLE Angiotensin converting enzyme homolog and therapeutic and diagnostic uses therefor	
JOURNAL Patent: US 6194556-A 3 27-FEB-2001;	
FEATURES Location/Qualifiers	
source 1..2415	
BASE COUNT 743 a 483 c 555 g 634 t	
ORIGIN /organism="unknown"	
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Score: 4291.00	Matches: 805
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
DB: 6	Gaps: 0
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QY 1 MetSerSerSerSerTrpLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20	
DB 1 ATGTCAAGCTCTTCCTGGCTCCTTCACGCCCTTGTCGTAACTGCTGCTCAGTCCACC 60	
QY 21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40	
DB 61 ATTGAGGAACAGCCCAAGACATTTTGGACAAGTTTAAACCACCAAGCCCAAGACCGTTTC 120	
QY 41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60	
DB 121 TATCAAGTTTCTACTGCTTCTTGGAAATTAACACCAATATTACTGAAGAGAAATGTCCAA 180	
QY 61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80	
DB 181 AACATGAATATGCTGGGACAAATGGTCTGCCTTTTAAAGGAACAGTCCACACTGGCC 240	
QY 81 GlnMetTrpProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnAlaLeu 100	
DB 241 CAATGTATTCACACAGAAATTCAGAAATCTCAGATCTCAGAGTTCAGTGCAGGCTCTT 300	
QY 101 GlnGlnAsnGlySerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120	
DB 301 CAGCAAAATGGGTCTTCAGTGTGTGAGAGACAGAGCAAGCGGTGAGCAACAATCTTA 360	
QY 121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140	
DB 361 AATACAATGAGCACCATCTACAGTACTGCGAAAAGTTTGTAAACCCAGATATCCACAAGAA 420	
QY 141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160	
DB 421 TGCTTATTAATTTGAACCCAGGTTTGAATGAAATAATGGCAACAGTTAGACTACAAATGAG 480	
QY 161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180	
DB 481 AGGCTCTGGCTTGGGAAAGCTGGAGATCTGAGGTGGCAAGCAGCTGAGGCCATTAATAT 540	
QY 181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200	
DB 541 GAAGAGTATGTGCTCTTGAATAATGAGATGGCAAGCAAAATCAATTATGAGACTATGGG 600	
QY 201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220	
DB 601 GAATTTGGAGGAGAGACTATCAAGTAAATGGGTAGATGGCTATGACTACAGCCCGCGC 660	
QY 221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240	
DB 661 CAGTTGATTGAAGATGTGCAACATACCTTTGAAGAGATTAACCAATATATGAACATCTT 720	
QY 241 HisAlaTyrValAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly 260	
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QY 281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300	
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DB 901 GCCTGGGATGCCACAGAGAAATATCAAGGAGGCCGAGAAGTCTTTGTATCTGTGGTCTT 960	
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DB 961 CCTAATATGACTCAGGATTTCTGGGAAATTTCCATGCTAACGGACCCAGGAAATGTTTCAG 1020	
QY 341 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360	
DB 1021 AAAGCAGTGTGCCATCCACAGCTTGGGACCTGGGAAGGCCGACTTCAGGATCCTTATG 1080	
QY 361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380	
DB 1081 TGCACAAAGGTGCATATGGACGACTTCTTGCACAGCTCATCTCAGATGGGCAATATCCAG 1140	
QY 381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400	
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QY 401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420	
DB 1201 CATGAAGCTGTGGGAAATCATGTCTCTTCTGACCCACACTAAGCAATTTAAATATCC 1260	
QY 421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440	
DB 1261 ATTGGTCTTCTGCACCCGATTTTCAAGAAGACAATGAAACAGAAATAAATCTCCTGCTC 1320	
QY 441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460	
DB 1321 AAACAAGCACTCACGATTTGTGGGACTCTGCCATTTACTTACATGTTAGAGAAAGTGGAGG 1380	
QY 461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480	
DB 1381 TGGATGCTCTTTAAAGGGNAATTTCCAAAGACCAGTGGATGAAAGTGGTGGGAGATG 1440	
QY 481 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500	
DB 1441 AAGCGAGAGATAGTTGGGTGGTGGAAACCTGTGCCCATGATGAAACATACTGTGACCCC 1500	
QY 501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrThrArgThrLeu 520	
DB 1501 GCATCTCTGTCCATGTTTCTAATGATTACTTCAATTCATTCGATATTACACAGGACCCCTT 1560	
QY 521 TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGlyProLeuHis 540	
DB 1561 TACCAATTCAGTTTCCAGAGCACATTTGTCAAGCAGCTAAACATGAGGCCCTCTGCAC 1620	
QY 541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560	
DB 1621 AAATGTGACATCTCAAACTCTCAGAAAGCTGCGAAGCTGCGAAGAACTGTTCATATGCTGAGGCTT 1680	
QY 561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580	
DB 1681 GGAAATCAGAACCCCTGGACCCCTAGCATTTGGAAATTTGTGTAGGACCAAGAACATGAAT 1740	
QY 581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600	
DB 1741 GTAAGCCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAACAAG 1800	
QY 601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620	
DB 1801 AATTCTTTTGTGGGATGGAGTACCGGACTGGAGTCCATATATGCAGACCAAGCAATCAAGTG 1860	

QY	621	ArgileSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet	640
Db	1861	AGGATAAGCCTAAATCAGCTCTTGGAGATAAGCATATGAATGAACGACAAATGAATG	1920
QY	641	TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn	660
Db	1921	TACCTCTTCGATCATCTGTTCATATGCTATGAGCAGTACTTTTAAAGTAAAAAT	1980
QY	661	GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer	680
Db	1981	CAGATGATCTTTTGGGGAGGAGATCTGCGAGTGGCTAAATTTGAAACCAAGAACTCC	2040
QY	681	PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal	700
Db	2041	TTTAATTTCTGTCTGCTGACCTGACCTAAATAATGTCTGATATCATCTTAGAACTGAAGTT	2100
QY	701	GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn	720
Db	2101	GAAGAGCCATCAGGATGTCGCGAGCCGTATCATGATGCTTCCGCTGAATGACAAAC	2160
QY	721	SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer	740
Db	2161	AGCCTAGAGTTTCTGGGGATACAGCAACACTTGGACCTCCTAACCAAGCCCTCTTCC	2220
QY	741	IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu	760
Db	2221	ATATGCTGATTTTGTGGAGTTGTGATGGAGTGTATGATGCTTGGCATTTGTCATCTG	2280
QY	761	IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro	780
Db	2281	ATCTTCACTGGATCAGATCGAAGAGAAATAATGAAGCAAGCTGGAGAAATCCT	2340
QY	781	TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp	800
Db	2341	TATGCTCCATCGATATTAGCAAGAGAAATAATCCAGATTCCAAACACATGATGAT	2400
QY	801	ValGlnThrSerPhe	805
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RESULT	2		
E43987			
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DEFINITION	E43987		
ACCESSION	E43987		
VERSION	E43987.1	GI:18629190	
KEYWORDS	JP 2001046072-A/1.		
SOURCE	unidentified.		
ORGANISM	unidentified.		
REFERENCE	1	(bases 1 to 2415)	
AUTHORS	Sugano, S. and Komatsu, T.		
TITLE	ACE-analogous gene		
JOURNAL	Patent: JP 2001046072-A 1	20-FEB-2001;	
COMMENT	OTSUKA PHARMACEUT CO LTD		
	OS	Unknown	
	PN	JP 2001046072-A/1	
	PD	20-FEB-2001	
	PF	06-AUG-1999	JP 1999223892
	PR		
	PI	SUMITO SUGANO, TAKAMI KOMATSU	
	PC	C12N15/09, A61K31/00, A61K31/7088, A61K38/00, A61K38/55,	
		A61K39/395, PC A61K39/395,	
	PC	A61K39/395, A61K48/00, A61P9/12, C07K14/47, C07K16/08, C12N1/15, PC	
		C12N1/19,	
	PC	C12N1/21, C12N5/10, C12Q1/68, G01N33/53, C12N15/00, A61K37/02, PC	
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	PC	C12N5/00	
	CC		
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FEATURES		Location/Qualifiers	

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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-635-501-2 (1-805) x E43987 (1-2415)			
QY	1	MetSerSerSerSerTrpLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr	20
Db	1	ATGTCGAAGCTCTTCCTGGCTCTTCTCAGCTTGTGCTTAAGTCTGCTCAGTCCACC	60
QY	21	IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe	40
Db	61	ATTGAGGAACAGGCCCAAGACATTTTGGACAAGTTTAACCAAGAGCCGAAGCTGTTC	120
QY	41	TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln	60
Db	121	TATCAAGTTTCCTTGGTCTTCTGGAAATTAACACCAATATTACTGAAGAAATGTCCAA	180
QY	61	AsnMetAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla	80
Db	181	AACATGAATAATGCTGGGGACAAATGGTCTGCTTTTAAAGGAACAGTCCACTTGCC	240
QY	81	GlnMetTrpProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnAlaLeu	100
Db	241	CAAATGATTCACACTACAGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTC	300
QY	101	GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu	120
Db	301	CAGCAAAATGGTCTTCAGTCTCTCAGAAAGACAGAGCAAGCGGTGAACACAAATCTA	360
QY	121	AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu	140
Db	361	AATACAATGAGCACCATCTACAGTACTGGAAAGTTTGTAAACCAATATCCACAAGAA	420
QY	141	CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTrpAsnGlu	160
Db	421	TGCTTATTACTTGAACACAGGTTTGAATCAATTAATGGCAACAGTTTAGACTCAATGAG	480
QY	161	ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr	180
Db	481	AGGCTCTGGGCTTGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATAT	540
QY	181	GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTrpGly	200
Db	541	GAAGATATCTGGTCTTGAANAATCAGATGGCAAGCAAAATCATTTATGAGGACTATGGG	600
QY	201	AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTrpSerArgGly	220
Db	601	GATTATTGGAGAGCAGACTATGAAGTAATGGGTAGATGGCTATGACTACAGCCGGGC	660
QY	221	GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu	240
Db	661	CAGTTGATTGAAGATGTGGACATACCTTTTGAAGAGATTAACCAATATATGAACATCTT	720
QY	241	HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly	260
Db	721	CATGCCATGTGAGGGCAAGTTGATCAATCCCTATCCTATATCATCATCAATTTGA	780
QY	261	CysLeuProAlaIleHisLeuLeuGlyAspMetTrpGlyArgPheThrAsnLeuTyrSer	280
Db	781	TGCCCTCCCTGCTCATTTGCTTGGTATGATTTGGGTAGATTTTGGACAAATCTGTACTCT	840
QY	281	LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln	300

Db 841 TTGACAGTTCCCTTTGGACAGAAACCAACATAGATGTTACTGATGCAATGGTGACACAG 900  
 QY 301 AlaTrpAspAlaGlnArgIlePheLysGluAlaGlnLysPheValSerValGlyLeu 320  
 Db 901 GCGTGGGATGCACAGAGATATTCAGAGGAGCCGAGAGATTCCTTGTGATCTGTTGGTCTT 960  
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 Db 1081 TGCACAAAGGTGACATGGAGCAGCTTCTGACAGCTCATCATGASATGGGCGATATCCAG 1140  
 QY 381 TyrAspMetAlaTrpAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400  
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 Db 1321 AAACAACCACTCAGATTTGGGACCTCTGCATTTACTTACATGTTAGAGAAAGTGGAGG 1380  
 QY 461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480  
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 QY 481 LysArgGluIleValGlyValGluProValProHisAspGluThrTyrCysAspPro 500  
 Db 1441 AAGCGAGAGATAGTTGGGGTGGTGGACCTGTGCCCTGATGATGAACATACATCTGACCCC 1500  
 QY 501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520  
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 QY 541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560  
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 QY 561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580  
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 QY 581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600  
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 QY 621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640  
 Db 1861 AGGATTAAGCCCTAAAAATCAGCTCTGGAGATAAAGCATATGAATGGACCGCAATGAATG 1920  
 QY 641 TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660

Db 1921 TACCTGTTCCGATCATCTGTTGCATATGCTATGAGGCGACTACTTTTAAAAAGTAAAAAT 1980  
 QY 661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680  
 Db 1981 CAGATGATCTTTTGGGAGGAGGATGCGAGTGGCTTAATTTGAACCAACAATCTCC 2040  
 QY 681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700  
 Db 2041 TTTAATTTCTTGTCTACCTGCACCTAAAAATGTGCTGATATCATCTCTAGAACTGAAGTT 2100  
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 Db 2341 TATGCTTCATCGATATTAGCAAGAGAGAAAAATAATCCAGATTTCCAAACACTGATGAT 2400  
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RESULT 3

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 ACCESSION E39033.1 GI:13017695  
 VERSION Jp 1999318472-A/1.  
 KEYWORDS Homo sapiens.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 2418)

AUTHORS

Christophe, D.S.N.N.

TITLE

MPROT15 polypeptide and MPROT15 polynucleotide

JOURNAL

Patent: JP 1999318472-A 1 24-NOV-1999;

COMMENT

OS Homo sapiens (human)  
 PN JP 1999318472-A/1  
 PD 24-NOV-1999  
 PF 22-JAN-1999 JP 1999014949  
 PR 13-MAY-1998 GB 9810373.2.18-AUG-1998 GB 9818009.4 PI  
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 PC C12N15/09, A61K31/00, A61K31/00, A61K31/00, A61K31/00, A61K31/70,  
 PC A61K38/00,  
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 PC G01N33/15,  
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 PC A61K37/02

CC key Location/Qualifiers  
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 FT source /organism="Homo sapiens (human)".

FEATURES

source

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BASE COUNT

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Alignment Scores:  
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Score: 4291.00 Matches: 805  
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US-09-635-501-2 (1-805) x E39033 (1-2418)

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QY	21	IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe	40
DB	61	ATTGAGGAACAGCCCAAGACATTTTGGACAAGTTTAACACCAAGCCGGAAGACCTGTTC	120
QY	41	TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln	60
DB	121	TATCAAGTTCACCTGCTTCCTGGAATATATACACCAATATTACTGAAGAGAAATGTC	180
QY	61	AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla	80
DB	181	AACATGAATAATGCTGGGACAAATGGTCTGCTCTTTTAAAGGAACAGTCCACACTGCC	240
QY	81	GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuAlaLeu	100
DB	241	CAAAATGATCCACTACAAGAAATTCAGAAATCTCACAGTCAAGCTTCAGCTGCAGGCTCT	300
QY	101	GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu	120
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QY	121	AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu	140
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QY	181	GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly	200
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DB	841	TTGACAGTTCCCTTTTGACACAGAAACCAACATAGATGTTACTGATGCAATGGTGGACC	900
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QY	601	AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal	620
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QY	661	GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer	680
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LOCUS E43988 ACE-analogous gene. 2599 bp DNA linear PAT 31-JAN-2002
DEFINITION ACE-analogous gene.
ACCESSION E43988
VERSION E43988.1 GI:18629191
KEYWORDS JP 2001046072-A/2.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2599)
AUTHORS Sugano,S. and Komatsu,T.
TITLE ACE-analogous gene
JOURNAL Patent: JP 2001046072-A 2 20-FEB-2001;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Unknown
PN JP 2001046072-A/2
PD 20-FEB-2001
PF 06-AUG-1999 JP 1999223892
PR
PI SUMIO SUGANO, TAKAMI KOMATSU
PC C12N15/09,A61K31/00,A61K31/7088,A61K38/00,A61K38/55,
A61K39/395, PC A61K39/395,
PC A61K39/395,A61K48/00,A61P9/12,C07K14/47,C07K16/08,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C1201/68,G01N33/53,C12N15/00,A61K37/02, PC
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 1 (bases 1 to 3325)  
 Donoghue,M., Hsieh,F., Baronas,E., Godbout,K., Gosselin,M.,  
 Stagliano,N., Donovan,M., Woolf,B., Robison,K., Jeyaseelan,R.,  
 Breitbart,R.E. and Acton,S.  
 A novel angiotensin-converting enzyme-related carboxypeptidase  
 (ACE2) converts angiotensin I to angiotensin 1-9  
 Circ. Res. 87 (5), E1-E9 (2000)  
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 Donoghue,M., Woolf,B., Robison,K. and Acton,S.  
 Direct Submission  
 Submitted (01-AUG-2000) Cardiovascular Biology, Millennium  
 Pharmaceuticals, Inc, 75 Sidney Street, Cambridge, MA 02139, USA  
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AUTHORS Tipnis,S.R., Hooper,N.M., Hyde,R., Karran,E., Christie,G. and Turner,A.J.  
TITLE A human homolog of angiotensin-converting enzyme. Cloning and functional expression as a captopril-insensitive carboxypeptidase  
J. Biol. Chem. 275 (43), 33238-33243 (2000)  
PUBMED 10924499  
REFERENCE 2 (bases 1 to 3405)  
AUTHORS Tipnis,S.R., Hooper,N.M., Hyde,R.J., Christie,G., Karran,E. and Turner,A.J.  
TITLE Direct Submission  
JOURNAL Submitted (02-MAR-2000) School of Biochemistry and Molecular Biology, University of Leeds, Mount Preston Street, Leeds, West Yorkshire LS5 9JT, UK  
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TITLE	Suzuki,Y., Watanabe,M. and Sugano,S. Cloning, expression analysis and chromosomal localization of a novel ACE like enzyme		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 2599)		
TITLE	Komatsu,T., Suzuki,Y. and Sugano,S. Direct Submission		
JOURNAL	Submitted (25-JUL-2000) Takami Komatsu, the Institute of Medical Science, Virology; 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:komatsui@ms.u-tokyo.ac.jp, Tel:81-3-5449-5283(ex.75283), Fax:81-3-5449-5416)		
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INQ TO INNOVATION TOUT THE CONVENTION

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Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
Direct Submission
Submitted (15-AUG-1999) MIPS, Am Klopferspitz 18a, D-82152
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de;
sequenced by AGORA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFp434A014) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
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## RESULT 11

E39034

LOCUS

DEFINITION

E39034

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

OS

PN

PD

PF

PR

CHRISTOPHER D SAZAN,NICOLA BAGESU

E39034 2262 bp DNA linear PAT 07-FEB-2001

MPROT15 polypeptide and MPROT15 polynucleotide.

E39034.1 GI:13017696

JP 1999318472-A/2.

Homo sapiens.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 2262)

Christopher, D.S.N.N.

MPROT15 polypeptide and MPROT15 polynucleotide

Patent: JP 1999318472-A 2 24-NOV-1999;

SMITHKLINE BEECHAM CORP PUBLIC LTD CO

OS Homo sapiens (human)

PN JP 1999318472-A/2

PD 24-NOV-1999

PF 22-JAN-1999 JP 1999014949

PR 13-MAY-1998 GB 9810373.2,18-AUG-1998 GB

9818009:4 PI

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VERSION AX047762.1 GI:11876768
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REFERENCE
1 (bases 1 to 2638)
AUTHORS Piddington,C.S., Petrie,C.R., Shoemaker,K.E. and Bishop,P.D.
TITLE zace2: a human metalloenzyme
JOURNAL Patent: WO 0070032-A 5 23-NOV-2000;
ZymoGenetics, Inc. (US)

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QY	781	TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp	800
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LOCUS			
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ACCESSION	AB053181	Mus musculus ACE2 mRNA for angiotensin-converting enzyme-related	ROD 03-APR-2001
VERSION	AB053181.1	carboxypeptidase, complete cds.	
KEYWORDS			
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ORIGIN

Alignment Scores:

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LOCUS AX047765
DEFINITION Sequence 8 from Patent WO0070032.
ACCESSION AX047765
VERSION AX047765.1 GI:11876771
KEYWORDS .
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Patent: WO 0070032-A 3 23-NOV-2000;  
 ZymoGenetics, Inc. (US)  
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DB	61	ATHGARGARGCARNARACNTYYTNGAYAAATTYAAYCAYGARGCNGARGAYTYNTTY	120
QY	41	TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln	60
DB	121	TAYCARWSNWSNTGCCNWSNTGGAAATYAAYACNAAYATHACNGARGAAYGTCNAR	180
QY	61	AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla	80
DB	181	AAATGCAAYAAAYGCGNGNGAYAAARTGWSNGCNTYYTNAARGARCARWSNACNTNGCN	240
QY	81	GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuAlaLeu	100
DB	241	CARATGTAYCCNTTNCARGARATHCARAAAYTTNACNGTNAARYTNCARYTNCARGCNTYN	300
QY	101	GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu	120
DB	301	CARCARAAYGGNWSNWSNTNTNWSNGARGAAYARWSNARMGNTYNAAYACNATHYTN	360
QY	121	AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu	140
DB	361	AAAYACNATGWSNACNATHYATWSNACNGGNAARGTNTGYAAYCNGAYAAAYCCNCARGAR	420
QY	141	CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu	160
DB	421	TGYTYNTYNTNGARCCNGGNTYNAAYGARATHATGCGNAAYWSNTNGAYTAYAAAYGAR	480
QY	161	ArgLeuTyrAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr	180
DB	481	MGNTYNTGGCCNTGGCARWSNTGCGNWSNGARGTNGGNARCARCYTNMGNCCTNTNTAY	540
QY	181	GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly	200
DB	541	GARGARTAYGTNGTNTNAARAAAYGARATGGCNGNGCNAAYCAVTAYGARGAYTAYGNN	600
QY	201	AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly	220
DB	601	GAYTAYTGGMGNGNGAYTAYGARGTNAAYCGGNGTNGAYGGNTAYGAYTAYWSNMGNGGN	660
QY	221	GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu	240
DB	661	CARYTNATHGARGAYGTNGARCAACNTTTCARGARATHAARCCNTYNTATYGARCAITYTN	720
QY	241	HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly	260
DB	721	CAYGCNTAYGTNMGNCNAARYTNATCAAYGCNTAYCCNWSNTAYATHWSNCCNATHGNN	780
QY	261	CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheThrIleThrAsnLeuTyrSer	280
DB	781	TGYTYTCCNGCNCAYTYTNTVNTNGNGAYATCTGGSGNMGNTTYTGACNAAYTYNTAYWSN	840
QY	281	LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln	300
DB	841	YTNACNGTNCCTNTTYGGNCARAAACCNAAATATHGAYGTNACNGAYGCNATGGTNGAYCAR	900

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Db 1981 CARATGATHYTNNTYGGNGARGAGYGTNMNGTNGCNAAYTNAARCCNMGNATHWSN 2040
QY 681 PheAsnPheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
Db 2041 TTYAATTTTGTACNGCCNCAARAAYGTNWSNGAYATHATCCNMGNACNGARGTN 2100
QY 701 GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720
Db 2101 GAFAARGCNATHMGNATGWSNMGNATHAAYGAYGCNTTYMGNTTYNAAYGAYAY 2160
QY 721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
Db 2161 WSNYTNAGRTTYTNGGNATHCARCCNACNTYNGNCCNCAAYCARCCNCCNGTNWSN 2220
QY 741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu 760
Db 2221 ATHTGGYTNATHGTNTTYGGNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGT 2280
QY 761 IlePheThrGlyIleArgAspArgLysLysLysLysLysLysLysLysLysLysLysLys 780
Db 2281 ATHTYACNGGNATHMGNAGYMGNAARAARAARAARAARAARAARAARAARAARAAYCCN 2340
QY 781 TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
Db 2341 TAYGCNWSNATHGAYATHWSNAARGGNGARAAYAYCCNGGNTTYCARAAYACNGAYGAY 2400
QY 801 ValGlnThrSerPhe 805
Db 2401 GTNCARACNWSNTTY 2415
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